

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/731,499

DATE: 02/26/97

TIME: 14:23:04

INPUT SET: S15759.raw #6

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

- 1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: GRAY, Joe W.  
6 COLLINS, Colin  
7 HWANG, Soo-In  
8 GODFREY, Tony  
9 KOWBEL, David  
10 ROMMENS, Johanna  
11  
12 (ii) TITLE OF INVENTION: GENES FROM THE 20q13 AMPLICON AND THEIR  
13 USES  
14  
15 (iii) NUMBER OF SEQUENCES: 44  
16  
17 (iv) CORRESPONDENCE ADDRESS:  
18 (A) ADDRESSEE: Townsend and Townsend and Crew  
19 (B) STREET: Two Embarcadero Center, 8th Floor  
20 (C) CITY: San Francisco  
21 (D) STATE: California  
22 (E) COUNTRY: USA  
23 (F) ZIP: 94111-3834  
24  
25 (v) COMPUTER READABLE FORM:  
26 (A) MEDIUM TYPE: Floppy disk  
27 (B) COMPUTER: IBM PC compatible  
28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
30  
31 (vi) CURRENT APPLICATION DATA:  
32 (A) APPLICATION NUMBER: US 08/731,499  
33 (B) FILING DATE: 16-OCT-1996  
34 (C) CLASSIFICATION:  
35  
36 (vii) PRIOR APPLICATION DATA:  
37 (A) APPLICATION NUMBER: US 08/680,395  
38 (B) FILING DATE: 15-JUL-1996  
39  
40 (viii) ATTORNEY/AGENT INFORMATION:  
41 (A) NAME: Hunter, Tom  
42 (B) REGISTRATION NUMBER: 38,498  
43 (C) REFERENCE/DOCKET NUMBER: 23070-068910  
44  
45 (ix) TELECOMMUNICATION INFORMATION:  
46 (A) TELEPHONE: (415) 576-0200

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/731,499

DATE: 02/26/97

TIME: 14:23:07

INPUT SET: S15759.raw

47 (B) TELEFAX: (415) 576-0300

48

49

50 (2) INFORMATION FOR SEQ ID NO:1:

51

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 3000 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

57

58 (ii) MOLECULE TYPE: cDNA

59

60

61 (ix) FEATURE:

62 (A) NAME/KEY: -

63 (B) LOCATION: 1..3000

64 (D) OTHER INFORMATION: /note= "cDNA clone 3bf4 of 3kb  
65 transcript of tyrosine kinase gene A6"

66

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

68

69 CCGCCGGCCG GGGCGCCTGG CTGCACTCAG CGCCGGAGCC GGGAGCTAGC GGCCGCCGCC 60

70

71 ATGTCCCACC AGACCGGCAT CCAAGCAAGT GAAGATGTTA AAGAGATCTT TGCCAGAGCC 120

72

73 AGAAATGGAA AGTACAGACT TCTGAAAATA TCTATTGAAA ATGAGCAACT TGTGATTGGA 180

74

75 TCATATAGTC AGCCTTCAGA TTCCTGGGAT AAGGATTATG ATTCCCTTTGT TTTACCCCTG 240

76

77 TTGGAGGACA AACAACCATG CTATATATTA TTCAGGTTAG ATTCTCAGAA TGCCCAGGGA 300

78

79 TATGAATGGA TATTCATTGC ATGGTCTCCA GATCATTTCTC ATGTTCGTCA AAAAATGTTG 360

80

81 TATGCAGCAA CAAGAGCAAC TCTGAAGAAG GAATTTGGAG GTGGCCACAT TAAAGATGAA 420

82

83 GTATTTGGAA CAGTAAAGGA AGATGTATCA TTACATGGAT ATAAAAAATA CTTGCTGTCA 480

84

85 CAATCTTCCC CTGCCCCACT GACTGCAGCT GAGGAAGAAC TACGACAGAT TAAAATCAAT 540

86

87 GAGGTACAGA CTGACGTGGG TGTGGACACT AAGCATCAAA CACTACAAGG AGTAGCATTT 600

88

89 CCCATTTCTC GAGAAGCCTT TCAGGCTTTG GAAAAATTGA ATAATAGACA GCTCAACTAT 660

90

91 GTGCAGTTGG AAATAGATAT AAAAAATGAA ATTATAATTT TGGCCAACAC AACAAATACA 720

92

93 GAACTGAAAG ATTTGCCAAA GAGGATTCCC AAGGATTCTG CTCGTTACCA TTTCTTTCTG 780

94

95 TATAAACATT CCCATGAAGG AGACTATTTA GAGTCCATAG TTTTATTTA TTCAATGCCT 840

96

97 GGATACACAT GCAGTATAAG AGAGCGGATG CTGTATTCTA GCTGCAAGAG CCGTCTGCTA 900

98

99 GAAATTGTAG AAAGACAAC TCAAATGGAT GTAATTAGAA AGATCGAGAT AGACAATGGG 960

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101	GATGAGTTGA	CTGCAGACTT	CCTTTATGAA	GAAGTACATC	CCAAGCAGCA	TGCACACAAG	1020
102							
103	CAAAGTTTTG	CAAAACCAAA	AGGTCCTGCA	GGAAAAAGAG	GAATTCGAAG	ACTAATTAGG	1080
104							
105	GGCCCAGCGG	AAACTGAAGC	TACTACTGAT	TAAAGTCATC	ACATTAAACA	TTGTAATACT	1140
106							
107	AGTTTTTTTAA	AAGTCCAGCT	TTTAGTACAG	GAGAACTGAA	ATCATTC CAT	GTTGATATAA	1200
108							
109	AGTAGGGAAA	AAAATTGTAC	TTTTTTGGAAA	ATAGCACTTT	TCACTTCTGT	GTGTTTTTAA	1260
110							
111	AATTAATGTT	ATAGAAGACT	CATGATTTCT	ATTTTTTGAGT	TAAAGCTAGA	AAAGGGTTCA	1320
112							
113	ACATAATGTT	TAATTTTGTC	ACACTGTTTT	CATAGCGTTG	ATTCCACACT	TCAAATACTT	1380
114							
115	CTTAAAATTT	TATACAGTTG	GGCCAGTTCT	AGAAAGCTCG	ATGTCTCAAA	GGGTAAACTT	1440
116							
117	ACTACTTTCT	TGTGGGACAG	AAAGACCTTA	AAATATTCAT	ATTACTTAAT	GAATATGTTA	1500
118							
119	AGGACCAGGC	TAGAGTATTT	TCTAAGCTGG	AACTTAGTG	TGCCTTGGAA	AAGCCGCAAG	1560
120							
121	TTGCTTACTC	CGAGTAGCTG	TGCTAGCTCT	GTCAGACTGT	AGGATCATGT	CTGCAACTTT	1620
122							
123	TAGAAATAGT	GCTTTATATT	GCAGCAGTCT	TTTATATTTG	ACTTTTTTTT	AATAGCATTA	1680
124							
125	AAATTGCAGA	TCAGCTCACT	CTGAAACTTT	AAGGGTACCA	GATATTTTCT	ATACTGCAGG	1740
126							
127	ATTTCTGATG	ACATTGAAAG	ACTTTAAACA	GCCTTAGTAA	ATTATCTTTC	TAATGCTCTG	1800
128							
129	TGAGGCCAAA	CATTTATGTT	CAGATTGAAA	TTTAAATTAA	TATCATTCAA	AAGGAAACAA	1860
130							
131	AAAATGTTGA	GTTTTAAAAA	TCAGGATTGA	CTTTTTTCTC	CAAAACCATA	CATTTATGGG	1920
132							
133	CAAATTGTGT	TCTTTATCAC	TTCCGAGCAA	ATACTCAGAT	TTAAAATTAC	TTTAAAGTCC	1980
134							
135	TGGTACTTAA	CAGGCTAACG	TAGATAAACA	CCTTAATAAT	CTCAGTTAAT	ACTGTATTTT	2040
136							
137	AAAACACATT	TAACTGTTTT	CTAATGCTTT	GCATTATCAG	TTACAACCTA	GAGAGATTTT	2100
138							
139	GAGCCTCATA	TTTCTTTGAT	ACTTGAAATA	GAGGGAGCTA	GAACACTTAA	TGTTTAATCT	2160
140							
141	GTTAAACCTG	CTGCAAGAGC	CATAACTTTG	AGGCATTTTC	TAAATGAACT	GTGGGGATCC	2220
142							
143	AGGATTTGTA	ATTTCTTGAT	CTAAACTTTA	TGCTGCATAA	ATCACTTATC	GGAAATGCAC	2280
144							
145	ATTTTCATAGT	GTGAAGCACT	CATTTCTAAA	CCTTATTATC	TAAGGTAATA	TATGCACCTT	2340
146							
147	TCAGAAATTT	GTGTTGAGT	AAGTAAAGCA	TATTAGAATA	ATTGTGGGTT	GACAGATTTT	2400
148							
149	TAAAATAGAA	TTTAGAGTAT	TTGGGGTTTT	GTTTGTTTAC	AAATAATCAG	ACTATAATAT	2460
150							
151	TTAAACATGC	AAAATAACTG	ACAATAATGT	TGCACTTGTT	TACTAAAGAT	ATAAGTTGTT	2520
152							

## INPUT SET: S15759.raw

153 CCATGGGTGT ACACGTAGAC AGACACACAT ACACCCAAAT TATTGCATTA AGAATCCTGG 2580  
154  
155 AGCAGACCAT AGCTGAAGCT GTTATTTTCA GTCAGGAAGA CTACCTGTCA TGAAGGTATA 2640  
156  
157 AAATAATTTA GAAGTGAATG TTTTCTGTGA CCATCTATGT GCAATTATAC TCTAAATTCC 2700  
158  
159 ACTACACTAC ATTAAAGTAA ATGGACATTC CAGAATATAG ATGTGATTAT AGTCTTAAAC 2760  
160  
161 TAATTATTAT TAAACCAATG ATTGCTGAAA ATCAGTGATG CATTTGTTAT AGAGTATAAC 2820  
162  
163 TCATCGTTTA CAGTATGTTT TAGTTGGCAG TATCATACCT AGATGGTGAA TAACATATTC 2880  
164  
165 CCAGTAAATT TATATAGCAG TGAAGAATTA CATGCCCTTCT GGTGGACATT TTATAAGTGC 2940  
166  
167 ATTTTATATC ACAATAAAAA TTTTCTCTCT TTAACAAAAA AAAACAAGAA AAAAAAAAAA 3000  
168  
169

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: -  
(B) LOCATION: 1..723  
(D) OTHER INFORMATION: /note= "cDNA clone 1b11 of 3.5kb transcript"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

190 TGGAAGCTGT CATGGTTACC GTCTCTAACG TTGGACTCTT AAGAAAATGA TTATTCCTGG 60  
191  
192 TTTCTAGACA GGCCAAATGT AATTCACCTA CGTGGCAGAT TAAAGAGGTG GGC'TTACTAG 120  
193  
194 ATTTGATTGG GTATTGAGCA TGCTCTGAAT GACAGTCCCC AAAAAGGACC TCTTATCCGT 180  
195  
196 TCTTCCCCTT GGGGAAGGGC TTTTGCCACT TCCATGTCAA TGTGGCAGTT GAGCTTGGAA 240  
197  
198 ATTGGTGCGT TGTACAACAT AAGCATTACT TCTCCAAGAT GTGCCTGTGT AGAAATGGTC 300  
199  
200 ATAGATTCAA AACTGTAGCT ACTATGTGGA CAGGGGGGCA GCAAGGACCC CACTTTGTAA 360  
201  
202 AACATGTTTT GGGGAATGT TTTGTTTTTC ATTTTCTTAT TACCTGGCAA AATAATCCAG 420  
203  
204 GTGGTGTGTG AGTCACCAGT AGAGATTATA AAGTCCAAGG AAGTAGAATC AGCCTTACAA 480  
205

## INPUT SET: S15759.raw

206 ACAGTGGACC TCAACGAAGG AGATGCTGCA CCTGAACCCA CWGAAGCGAA ACTCAAAAGA 540  
207  
208 GAAGAAAGCA AACCAAGAAC CTCTCTGATG RCGTTTCTCA GACAAATGGT AAGCCCCCTTA 600  
209  
210 CTTCCAGTAT AGGAAACCTA AGATACCTAG AGCGGCTTTT GGGAACAATG GGCTCATGCC 660  
211  
212 ACAGGTAGTA GGAGACATAA TTGTAGCTGG TGTGTATGGA ATGTGAATGG AATATGGATT 720  
213  
214 GCG 723  
215  
216

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

220 (A) LENGTH: 1507 base pairs  
221 (B) TYPE: nucleic acid  
222 (C) STRANDEDNESS: single  
223 (D) TOPOLOGY: linear  
224

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

229 (A) NAME/KEY: -  
230 (B) LOCATION: 1..1507  
231 (D) OTHER INFORMATION: /note= "cDNA clone cc49 of 6-7kb  
232 transcript with homology to C2H2 zinc  
233 finger genes"  
234  
235

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

236  
237  
238 GCAGGTTGCT GGGATTGACT TCTTGCTCAA TTGAAACACT CATTC AATGG AGACAAAGAG 60  
239  
240 CACTAATGCT TTGTGCTGAT TCATATTTGA ATCGAGGCAT TGGGAACCCCT GTATGCCTTG 120  
241  
242 TTTGTGGAAA GAACCAAGTGA CACCATCACT GAGCTTCCTA AAAGTTCGAA GAAGTTAGAG 180  
243  
244 GACTATACAC TTTCTTTTGA ACTTTTATAA TAAATATTTG CTCTGGTTTT GGAACCCAGG 240  
245  
246 ACTGTTAGAG GGTGAGTGAC AGGTCTTACA GTGGCCTTAA TCCAACCTCA GAAATTGCCC 300  
247  
248 AACGGAACCT TGAGATTATA TGCAATCGAA AGTGACAGGA AACATGCCAA CTCAATCCCT 360  
249  
250 CTTAATGTAC ATGGATGGCC AAGAGTGATT GGCAGCTCTC TTGCCAGTCC GATGGAGATG 420  
251  
252 GAGATGCCTT GTCAATGAAA GGGCCCNCTG TTGTCAATTC CGAGCTACAC AAAGAAAAAA 480  
253  
254 ATGTCAATCC GAATCGAGGG GAATATGCCC TTGGATTGCA TGTCTGTCAG CCAGACCTTC 540  
255  
256 ACACATTGAG AAGACCTTAA TAAACATGTC TTAATGCAAC ACCGGCCTAC CCTCTGTGAA 600  
257  
258 CCAGCAGTTC TTCGGGTTGA AGCAGAGTAT CTCAGTCCGC TTGATAAAAG TCAAGTGCGA 660

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/731,499**

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Original Text